

[illegible]

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 17, 2005, 16:48:20 ; Search time 40 Seconds
(without alignments)
673.517 Million cell updates/sec

Title: US-10-680-349-42
Perfect score: 1462
Sequence: 1 MNYKKILVRSALISLMSILP.....ASVTLDVGVFGGIGMRFTF 280

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	629.5	43.1	276	2	JE0218	28k surface antige
2	620	42.4	286	2	JE0219	28k surface antige
3	603	41.2	280	2	JE0217	28k surface antige
4	583	39.9	278	2	JE0216	major antigenic pr
5	565	38.6	284	2	I40882	28k surface antige
6	515.5	35.3	287	2	JE0220	major surface prot
7	386.5	26.4	282	2	I39648	28k surface antige
8	227.5	15.6	133	2	JE0221	heat resistant agg
9	119.5	8.2	264	2	I54668	probable outer mem
10	107.5	7.4	239	2	AH0541	hemolysin A precu
11	104.5	7.1	738	2	S01892	DNA-directed RNA p
12	102	7.0	1176	2	A27826	3-oxoacyl-l-acyl-ca
13	101.5	6.9	415	2	B70448	adhesin homolog lm
14	100	6.8	1582	2	AC1153	hypothetical prote
15	98	6.7	3890	2	C89921	heat resistant agg
16	97.5	6.7	274	2	AC3295	DNA-directed RNA p
17	97.5	6.7	1174	2	S28976	glutamate rich pro
18	97.5	6.7	1271	2	A45555	glycosidase homolo
19	97.5	6.7	1310	2	AD1380	outer cell wall pr
20	95	6.5	1004	2	B25039	peptidoglycan boun
21	95	6.5	1578	2	AD1512	6-Phospho-Beta-D-G
22	94.5	6.5	474	2	F97264	endo-beta-N-acetyl
23	93.5	6.4	658	2	E95111	hypothetical prote
24	93	6.4	180	2	F71639	hypothetical prote
25	93	6.4	608	2	H64473	hypothetical prote
26	93	6.4	745	2	T51370	conserved hypotet
27	92.5	6.3	219	2	AF2658	hypothetical prote
28	92.5	6.3	219	2	C97440	hypothetical prote
29	92.5	6.3	401	2	F86754	prophage pi2 prote

30	92.5	6.3	585	2	C69336	probable electron
31	91.5	6.3	721	2	C97980	endo-beta-N-acetyl
32	91.5	6.3	1224	2	A25884	DNA-directed RNA p
33	91.5	6.3	1635	2	AI0452	hemolysin [importe
34	91	6.2	282	2	S16617	opacity protein op
35	91	6.2	588	2	AG0517	penicillin-binding
36	91	6.2	1348	2	B23496	TyB protein - years
37	91	6.2	1598	2	S69967	TyB protein - years
38	91	6.2	1770	2	S69953	TyB protein - years
39	91	6.2	1770	2	S86551	TyB protein - years
40	91	6.2	1770	2	S70233	TyB protein - years
41	91	6.2	1770	2	S69966	TyB protein - years
42	91	6.2	1770	2	S69950	TyB protein - years
43	91	6.2	1770	2	S70230	TyB protein - years
44	91	6.2	1771	2	S53592	TyB protein - years
45	91	6.2	1810	2	S69973	TyB protein - years

ALIGNMENTS

RESULT 1
JE0218
28k surface antigen 5 - Ehrlichia chaffensis
N;Alternate names: MAP1
C;Species: Ehrlichia chaffensis
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C;Accession: JE0218
R;Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.
Biochem. Biophys. Res. Commun. 247, 636-643, 1998
A;Title: Molecular characterization of a 28kDa surface antigen gene family of the tribe
A;Reference number: JE0216; MUID:98321180; PMID:9647746
A;Accession: JE0218
A;Molecule type: DNA
A;Residues: 1-276 <RED>
A;Cross-references: UNIPROT:Q93DD2; UNIPROT:Q9ACI9; GB:AF062761

Query Match 43.1%; Score 629.5; DB 2; Length 276;
Best Local Similarity 47.9%; Pred. No. 8.3e-44;
Matches 137; Conservative 41; Mismatches 87; Indels 21; Gaps 6;

Qy	1	MNYKKILVRSALISLMSILPQSPADPVGSRDNDKEGFIYSKYNPSISHPKFSAEET	60
Db	1	MNYKKVFIITSAIISLISLFGVSFSDPAGSGINGN---FYISGKYMPSASHFGVPSAKE-	56
Qy	61	PINGTSLTKKVFGLKKQGD-----ITKKDDTRVAPGIDFONNLISFGSGSIGYSMDG	114
Db	57	-----ERNTTVGVFGLKQNDGSAISNSPNDVFTVSNYSFKYENNPFLGAGALIGSMDG	112
Qy	115	PRIELEAAVQOQNPQNTDNDNGEYKHFALSRKDAME----DQOYVVLKNDGITFMS	170
Db	113	PRIELEVSVEYTFDVKQGN--YKNEAHRYCALSHNSAADMSSANNFVFLKNEGLLDIS	170
Qy	171	LMVNTCYDITABGVSVFPVACAGIGADLITIPKDLNLFKAYQKIGISYIPTEVVSFIG	230
Db	171	FMLNACVDVVGEIGIPFSPYICAGIGTDLVSMPEATNPKISYQKGLGISYISPEASVFIG	230
Qy	231	GYHGVIGNKFEKIPVITPVVLDAPQ--TTSASVTLDVGVGGEIG	275
Db	231	GHFHKVIGNEFRDIPTIITPGTSLAGKNYPALVILDVCHFGIEMG	276

RESULT 2
JE0219
28k surface antigen 2 - Ehrlichia chaffensis
N;Alternate names: MAP1
C;Species: Ehrlichia chaffensis
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C;Accession: JE0219
R;Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.
Biochem. Biophys. Res. Commun. 247, 636-643, 1998
A;Title: Molecular characterization of a 28kDa surface antigen gene family of the tribe
A;Reference number: JE0216; MUID:98321180; PMID:9647746

A;Accession: JE0219
A:Molecule type: DNA
A;Residues: 1-286 <RED>
A;Cross-references: UNIPROT:O52105; GB:AF062761

Query Match 42.4%; Score 620; DB 2; Length 286;
Best Local Similarity 47.3%; Pred.No.5.2e-43;
Matches 139; Conservative 42; Mismatches 89; Indels 24; Gaps 7;

Qy 1 MNKKILVRSALISLMSILPQCSPADPPGSRITNDNKEG-FYISAKYNPSISHFRKFSABE 59
Db :|::||::||::||::||::||::||::||::||::||::||::||::||:
1 MNCEKFPTTTALTLLMSPFGISSLSDPV--QQDNISGNFYISGYMPFSASHGFVSACE 57
Qy 60 TPINGTNSLTKKVFGLKKDGD-----ITKKDDFTTRVAPGIDFQNLIISGPSGSIGYSMD 113
Db :|::||::||::||::||::||::||::||::||::||::||::||::||:
58 -----ERNTTGVVGIEQDWRCVISRTTLSDIFTPVPNYSFKYENNLFSGAGATGYSMD 112
Qy 114 GPRIELEAAAYQFPNPNTDNNDTNGEYYKHFFALSRRKDAMEDQ-----QVVVLKNDDGIT 167
Db :|::||::||::||::||::||::||::||::||::||::||::||::||:
113 GPRIELEVSVEAFDPVKNOGNN--YKNEAHRYVALSHLGTTETQDCGASASVFLINEGILL 170
Qy 168 FMSLMWNTCYDITRAGVSFVYPACAGIGADIITTIPKOLNLKPAYOGKTGISYPTPEVSA 227
Db :|::||::||::||::||::||::||::||::||::||::||::||::||:
171 DKSEPLNACYDVISEGIPFPSYICAGIGIDLVSFEAINPKISYQGKLGLSYIPSPEASV 230
Qy 228 FIGVHYHGVINKEEKIVPIVTVLVNDAPO-TTSASVTLDVGYFGEGTGMRFTF 280
Db :|::||::||::||::||::||::||::||::||::||::||::||::||:
231 FIGHFHKVIGNERFDIPTMPISESALACKGNYPATVILDVYFIGIELGGRFNF 284

RESULT 3
JE0217
28k surface antigen 4 - Ehrlichia chaffensis
N;Alternate names: MAP1
C;Species: Ehrlichia chaffensis
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C;Accession: JE0217
R;Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.
Biochem. Biophys. Res. Commun. 247, 636-643, 1998
A>Title: Molecular characterization of a 28kDa surface antigen gene family of the tribe
A;Reference number: JE0216; MUID:98321180; PMID:9647746
A;Accession: JE0217
A:Molecule type: DNA
A;Residues: 1-280 <RED>
A;Cross-references: UNIPROT:O52107; GB:AF062761

Query Match	41.2%	Score 603;	DB 2;	Length 280;
Best Local Similarity	45.1%	Pred. No. 1.2e-41;		
Matches 133;	Conservative 54;	Mismatches 79;	Indels 30;	Gaps 10;
Qy	1	MNYKKILVRSALISLMSILPQSGFADPVGSGTNDNKEG-FYISAKYNPDSIHHPRKFSABE	59	
Db	1	MNCKKFPITTTLVLSLMSPLGISPSDAV---QNDNVGNGFYISGKYVPSVSHFGVFSAKQ	57	
Qy	60	TPINGTNSLTKVKGLKDGQ--ITTKD-DFTVAPGIDF--QNNLISGSGSGTGYGMD	113	
Db	58	-----ERNTTIGVGLQDWDGSGTISKNSPENTFVNPYSPKYEINPFLGFAVAGVLYMN	112	
Qy	114	GPRIELEAAVQFNPQNTDNDNTONGEYXKHFALSR-----KDAMEDQQVYVLKNDGIGTFM	169	
Db	113	GPRIELEMSYETFDVKQCGNNYKDA--HKYYALTHNSGGKLSNAGDKFVFLKNEGLLDI	170	
Qy	170	SLMWNTCYDITAEGVSVFPYACAGIGADLITIFKDLNLKFAYQGGKIGHSYIPITPEVSAFI	229	
Db	171	SLMLNACVDVISEGIPFSPYICAGVGTDLISMFPAINPKISYQCKGLSYSISPEASVFV	230	
Qy	230	GGYTHGVIGNKPEKIPITPVVLNDAPOTTGAS-----VTLDVGYFGBIGMRFTF	280	
Db	231	GGHPHKVIGNEFRDIPAMIP-----SYSTLGNHFTITVLSGVCHFGVBLGRGNF	280	

RESULT 4
JE0216

28k surface antigen family of the tribe I

N;Alternate names: MAP1
C/Species: Ehrlichia chaffeensis
C/Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C/Accession: JE0216
R;Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.
Biochem. Biophys. Res. Commun. 247, 636-643, 1998
A/Title: Molecular characterization of a 28kDa surface antigen gene family of the tribe I
A/Reference number: JE0216; MUID:98321180; PMID:9647746
A/Accession: JE0216
A/Molecule type: DNA
A/Residues: 1-278 <RED>
A/Cross-references: UNIPROT:O52106; GB:AF062761

Query Match 39.9%; Score 583; DB 2; Length 278;
Best Local Similarity 43.6%; Pred. No. 5.1e-40;
Matches 126; Conservative 49; Mismatches 94; Indels 20; Gaps 7;

Qy 1 MNVKKILVRGALISLMSILPYQSADPVGSRTNDNKEG-FYISAKYNPSISHFRKFSAE 59
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 1 MNCKKPFITTAIVSLMSFLPGISFSDPV--QGDNISGNFYVGKYMPASAHFGMFSAXE 57
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Qy 60 TPINGTNSLTFFKVGLKGD-----GDITKDDDFTRVAFGIDFQNNLISGFSGSIGYSMDG 114
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 58 -----EKNPVTALYGLKDWEGISSSSHNDHFNKNKGYSFKYENPNPFLGFAAGIYSMG 112
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Qy 115 PRJLEAAAYQQFPNKNTDNDNGEYVKHFALSRKD--AMEDQYYVLKNDGITFMSL 171
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 113 PRVEFEVSYTEFDVQNOGNNYKDA--HRYCALGOODNSGTPKTSKYVLLKSEGLLDISF 170
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Qy 172 MVNTCYDITAEGSVFVPACAGIGADLITIPLDLMLKPAYQGIKIGSYPIITEVSAPIGG 231
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 171 MLNACYDIINESIPLSPVICAGVGTDLISMPEATNPKISYQGLGLSYINPEASVFIMG 230
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Qy 232 YYHCVIGNKREKIPVIPTVPLNDAPQTTSASVTLTDVGYFCGEIGHRFTF 280
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 231 HFHKVIGNEPRDPTLKAFVTSSATPOL-AIVTLVCHFGIELGGREFNF 278
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

RESULT 5
I40882
major antigenic protein - heartwater rickettsia
C/Species: Cowdria rumenantium (heartwater rickettsia)
C/Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C/Accession: I40882; S42827
R;van Vliet, A.H.; Jongejans, F.; van Kleef, M.; van der Zeijst, B.A.
Infect. Immun. 62, 1451-1456, 1994
A/Title: Molecular cloning, sequence analysis, and expression of the in
A/Reference number: I40882; MUID:94178956; PMID:8132352
A/Accession: I40882
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-284 <RES>
A/Cross-references: UNIPROT:Q46327; EMBL:X74250; NID:g454266; PIDN:CRA52309.1; PID:g454266
C/Genetics:
A/Gene: map1

[illegible]

```
Qy 168 FMSLMVNTCYDITAEVGFVFPYACAGIGADLITIFKDLNLKFAVQKIGISYPITPEVSA 227
Db 168 DISLMLNACYDIDLMDPVPFVYVACAGITDLVSVINATNPKLSYQKGLGISYINPEASI 227
Qy 228 FIGGYHGVIGNKPEKIPVITPVVNLNDAPQTTSS-----ASVTLDVGYFGGEIGMRFTF 280
Db 228 FIGGHFRVIGNEPKDI--ATSKVFTSSGNASSAVSPGASAILDVCHFGIEIGGRVVF 284

RESULT 6
JE0220
28k surface antigen 1 - Ehrlichia canis
C;Species: Ehrlichia canis
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C;Accession: JE0220
R;Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; BurrIDGE, M.J.; Alleman, A.R.
Biochem. Biophys. Res. Commun. 247, 636-643, 1998
A;Title: Molecular characterization of a 28kDa surface antigen gene family of the tribe
A;Reference number: JE0216; MUID:98321180; PMID:9647746
A;Accession: JE0220
A;Molecule type: DNA
A;Residues: 1-287 <RED>
A;Cross-references: UNIPROT:Q9ZGJ0; GB:AF062762; NID:g3327964; PIDN:AAC26721.1; PID:g3327964

Query Match 35.3%; Score 515.5; DB 2; Length 287;
Best Local Similarity 39.3%; Pred. No. 1.7e-34;
Matches 120; Conservative 47; Mismatches 95; Indels 43; Gaps 7;

Qy 1 MNYKILVRGALISLMSILPQSPADPVGSRRTNDKGEFVISAQNPISISHFRKFSAEET 60
Db 1 MNYKKTITVALVLTSTFTIFIPYSPARASTHN----FTISGKMTASHFGIFSAGE- 56
Qy 61 PINGTNSLTKKVFGKL--KKDGDITKDDFTRVAP-----GIDFQNNLISFGSGISGYSDMG 114
Db 57 ----EQSFTKVLVGLDQRLSHNINNDTAKSLKQVNSPKYKUNPFLGPAAGIAGYSIGN 112
Qy 115 PRIELEYAAYQOFPNPKNTDNN-----DTDNGEYKHFALSRKDMED 155
Db 113 SRIELEYSHIFDTKPNNGNLYLNDSHKICALSHGSHCSGDSGDWY-----TAKT 163
Qy 156 QOVVLKNDGITFMSLMVNTCYDITAEVGFVFPYACAGIGADLITIFKDLNLKFAVQGI 215
Db 164 DKFVLLKNEGLLDVSMFNACYDITTEKMPFSPYICAGITDLSIMFETTONKISYQGL 223
Qy 216 GISYPTPEVSAFISGYYHGVIGNKPEKIPVITPVVNLNDAPQTTSSASVTLDVGYFGGEIG 275
Db 224 GLNTINSRVSVFAGGHFHKVIGNEFKGIPITLLPDGSGNIQV-QSATVTLDVCHFGIEIG 282
Qy 276 MRTPF 280
Db 283 SRPFF 287

RESULT 7
I39648
major surface protein 4 - Anaplasma marginale
C;Species: Anaplasma marginale
C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C;Accession: I39648
R;Oberle, S.M.; Barbet, A.F.
Gene 136, 291-294, 1993
A;Title: Derivation of the complete map4 gene sequence of Anaplasma marginale without cl
A;Reference number: I39648; MUID:94124017; PMID:8294020
A;Accession: I39648
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-282 <RES>
A;Cross-references: UNIPROT:Q07408; GB:L01987; NID:gl142174; PIDN:AAC36877.1; PID:gl142175
C;Genetics:
A;Gene: map4

Query Match 26.4%; Score 386.5; DB 2; Length 282;
Best Local Similarity 32.2%; Pred. No. 5.1e-24;
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Matches 96; Conservative 54; Mismatches 113; Indels 35; Gaps 9;
Qy 1 MNYKIL--VRSALISLMSILPQSPADPVGSRRTNDKGEFVISAQNPISISHFRKFSAEET 49
Db 1 MNYRELFTGSLSAATVCACSLLVSGAVVAPSPMSHEVASEGVGSGSPYVGAAYSPAPFSV 60
Qy 50 SHP--RKFSAEETPINGTNSLTKKVFGKLKDDITKDDFTRVAPGIDFQNNLISFGSGS 107
Db 61 TSFDMRESSKETSVRGYDKSIATI-----DVSVPANFSKGYTTFAPFKNLITSFDGA 113
Qy 108 IGYSDMGPRIELEYAAYQOFPNPKNTDNDTNGEYKHFALSRKDMEDQOYVVLK 162
Db 114 VGSISGLGARVELASVRRP-----ATLDGQVAKSGAESLAITRDANITENYFVVK 166
Qy 163 NDGITFMSLMVNTCYDITAEVGFVFPYACAGIGADLITIFKDLNLKFAVQKIGISYPIT 222
Db 167 IDEITNTSVMLNGCYDVLHDTLPVSPVVCAGIGASFDVDSKQVTTKLAYRGKVGISYQFT 226
Qy 223 PEVSATFIGGYHGVIGNKPEKIPVITPVVNLNDAPQTTSSASVTLDVGYFGGEIGMRTPF 280
Db 227 PEISLVAGGFYHGLFDESXYKDI PAHNSVKFSG---EAKASVKAKHADIYGFNLGARPLF 281

RESULT 8
JE0221
28k surface antigen 2 - Ehrlichia canis
C;Species: Ehrlichia canis
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C;Accession: JE0221
R;Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; BurrIDGE, M.J.; Alleman, A.R.
Biochem. Biophys. Res. Commun. 247, 636-643, 1998
A;Title: Molecular characterization of a 28kDa surface antigen gene family of the tribe
A;Reference number: JE0216; MUID:98321180; PMID:9647746
A;Accession: JE0221
A;Molecule type: DNA
A;Residues: 1-133 <RED>
A;Cross-references: UNIPROT:O85360; GB:AF062762; NID:g3327964; PIDN:AAC26722.1; PID:g3327964

Query Match 15.6%; Score 227.5; DB 2; Length 133;
Best Local Similarity 41.4%; Pred. No. 1.6e-11;
Matches 59; Conservative 20; Mismatches 49; Indels 13; Gaps 4;

Qy 1 MNYKILVRGALISLMSILPQSPADPVGSRRTNDKGEFVISAQNPISISHFRKFSAEET 60
Db 1 MNCKQVFTTISALISSIYFLENVSYPNVYG--NSMTGNFYISGKMPSPVPHGIFSABE- 57
Qy 61 PINGTNSLTKKVFGKLKDDITKDDFTRVAPGIDFQNNLISFGSGISGYSDMG 114
Db 58 ----EKKKTTVVYGLKENWAGDAISSQSPDDNFTIRNYSFKYASNKFLGFAVAIGYSIGS 113
Qy 115 PRIELEYAAYQOFPNPKNTDNN 134
Db 114 PRIEVEVMSYEAQFDVKQGNV 133

RESULT 9
I54668
heat resistant agglutinin 1 - Escherichia coli
C;Species: Escherichia coli
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C;Accession: I54668; MUID:169133; I69134
R;Lutwyche, P.; Rupp, R.; Cavanagh, J.; Warren, R.A.; Brooks, D.E.
Infect. Immun. 62, 5020-5026, 1994
A;Title: Cloning, sequencing, and viscometric adhesion analysis of heat-resistant agglut
A;Reference number: I54668; MUID:95012721; PMID:7927783
A;Accession: I54668
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-264 <RES>
A;Cross-references: UNIPROT:Q46678; EMBL:U07174; NID:g463910; PIDN:AAC13751.1; PID:g463910
A;Accession: I69133
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
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